

## SEQUENCE LISTING

&lt;110&gt; AKZO Nobel N.V.

&lt;120&gt; Shiga-like toxin vaccine

&lt;130&gt; 2003.006

&lt;160&gt; 4

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 1325

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(954)

&lt;400&gt; 1

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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser	
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acc cct ctt gaa cat ata tct cag gga gct aca tct gta tcc gtt att	192
Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile	
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Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu	
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gat gtt tat cag gag cgt ttt gac cat ctt cgt ctg att att gaa cga	288
Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg	
85 90 95	
aat aat tta tat gtg gct gga ttt gtt aat acg aca aca aat act ttc	336
Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr Asn Thr Phe	
100 105 110	
tac aga ttt tca gat ttt gca cat ata tca ttg ccc ggt gtg aca act	384
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr	
115 120 125	
att tcc atg aca acg gac agc agt tat acc act ctg caa cgt gtc gca	432
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala	
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gcg ctg gaa cgt tcc gga atg caa atc agt cgt cac tca ctg gtt tca	480
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser	
145 150 155 160	
tca tat ctg gcg tta atg gag ttc agt ggt aat aca atg acc aga gat	528
Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp	
165 170 175	
gca tca aga gca gtt ctg cgt ttt gtc act gtc aca gca gaa gcc tta	576

## 2

Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu  
180 185 190

cgg ttc agg caa ata cag aga gaa ttt cgt ctg gca ctg tct gaa act 624  
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr  
195 200 205

gct cct gtt tat acg atg acg ccg gaa gac gtg gac ctc act ctg aac 672  
Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn  
210 215 220

tgg ggg aga atc agc aat gtg ctt ccg gag tat cgg gga gag gct ggt 720  
Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly  
225 230 235 240

gtc aga gtg ggg aga ata tcc ttt aat aat ata tca gcg ata ctt ggt 768  
Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly  
245 250 255

act gtg gcc gtt ata ctg aat tgt gga aat tca tca aga aca atc aca 816  
Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr  
260 265 270

ggg gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc 864  
Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu  
275 280 285

agg gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag 912  
Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln  
290 295 300

tca gag gtt gac ata tat aac aga att cgg gat gaa tta tga 954  
Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu  
305 310 315

ataaagtaaa atgttatgtt ttatttacgg cgttactatc ctctctatat gcacacggag 1014

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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser  
35 40 45

Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile  
 50 55 60

Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu  
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Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg  
 85 90 95

Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr Asn Thr Phe  
 100 105 110

Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr  
 115 120 125

Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala  
 130 135 140

Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser  
 145 150 155 160

Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp  
 165 170 175

Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu  
 180 185 190

Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr  
 195 200 205

Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn  
 210 215 220

Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly  
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Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly  
 245 250 255

Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr  
 260 265 270

Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu  
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 gtatccgtta ttaatcatac accaccagga agttatatct ccgtaggtat acgaggggctt 240  
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 Lys Val Lys Cys Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser Leu Tyr  
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 gca cac gga gct ccc cag act att aca gaa cta tgt tcg gaa tat cgc 1052  
 Ala His Gly Ala Pro Gln Thr Ile Thr Glu Leu Cys Ser Glu Tyr Arg  
 20 25 30  
 aac aca caa ata tat acg ata aat gac aag ata cta tca tat acg gaa 1100  
 Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr Thr Glu  
 35 40 45 50  
 tcg atg gca ggc aaa aga gaa atg gtt atc att aca ttt aag agc ggc 1148  
 Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys Ser Gly  
 55 60 65  
 gaa aca ttt cag gtc gaa gtc ccg ggc agt caa cat ata gac tcc cag 1196  
 Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln  
 70 75 80  
 aaa aaa gcc att gaa agg atg aag gac aca tta aga atc aca tat ctg 1244  
 Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr Tyr Leu

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aat tca att gcg gca atc agt atg aaa aac tag      1325
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              20              25              30

Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
      35              40              45

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
 50              55              60

Ser Gly Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
65              70              75              80

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
              85              90              95

Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
      100              105              110

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Lys Asn
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